

## WEST Search History

DATE: Saturday, August 19, 2006

<u>Hide?</u>	<u>Set Name</u>	<u>Query</u>	<u>Hit Count</u>
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		<i>DB=PGPB,USPT; PLUR=YES; OP=ADJ</i>	
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<input type="checkbox"/>	L1	(T1R2 and T1R3).clm.	20
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END OF SEARCH HISTORY

GenCore version 5.1.9  
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OM protein - protein search, using sw model

Run on: June 20, 2006, 18:11:56 ; Search time 188 Seconds  
(without alignments)  
2067.219 Million cell updates/sec

Title: US-10-035-045-21  
Perfect score: 4443  
Sequence: 1 MGPRAKTICSLFFLLWVLAE.....ERNTPAYFNSMIQGYTMRRD 839

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published\_Applications\_AA\_Main:\*  
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4: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10A\_PUBCOMB.pep:\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	4443	100.0	839	3	US-09-897-427A-4	Sequence 4, Appli
2	4443	100.0	839	4	US-10-035-045-21	Sequence 21, Appl
3	4443	100.0	839	4	US-10-179-373-6	Sequence 6, Appli
4	4443	100.0	839	4	US-10-725-103-6	Sequence 6, Appli
5	4443	100.0	839	4	US-10-725-489-6	Sequence 6, Appli
6	4443	100.0	839	4	US-10-725-080A-6	Sequence 6, Appli
7	4443	100.0	839	4	US-10-725-472A-6	Sequence 6, Appli
8	4443	100.0	839	4	US-10-725-276-21	Sequence 21, Appl
9	4443	100.0	839	4	US-10-770-127-198	Sequence 198, App
10	4443	100.0	839	5	US-10-725-284-21	Sequence 21, Appl
11	4443	100.0	839	5	US-10-725-418-6	Sequence 6, Appli
12	4443	100.0	839	5	US-10-679-102-29	Sequence 29, Appl
13	4443	100.0	839	5	US-10-725-475-6	Sequence 6, Appli
14	4443	100.0	839	6	US-11-050-804-4	Sequence 4, Appli
15	4422	99.5	839	4	US-10-246-785-4	Sequence 4, Appli
16	4392.5	98.9	838	3	US-09-927-315-9	Sequence 9, Appli
17	4392.5	98.9	838	4	US-10-190-417-9	Sequence 9, Appli
18	4392.5	98.9	838	5	US-10-679-102-9	Sequence 9, Appli
19	4392.5	98.9	838	5	US-10-645-441-9	Sequence 9, Appli
20	3463.5	78.0	669	4	US-10-124-598-7	Sequence 7, Appli
21	3463.5	78.0	669	4	US-10-096-144-7	Sequence 7, Appli
22	3463.5	78.0	669	4	US-10-225-567A-683	Sequence 683, App
23	3231	72.7	843	3	US-09-927-315-7	Sequence 7, Appli
24	3231	72.7	843	4	US-10-124-598-1	Sequence 1, Appli
25	3231	72.7	843	4	US-10-096-144-1	Sequence 1, Appli
26	3231	72.7	843	4	US-10-246-785-6	Sequence 6, Appli
27	3231	72.7	843	4	US-10-190-417-7	Sequence 7, Appli
28	3231	72.7	843	4	US-10-179-373-17	Sequence 17, Appl
29	3231	72.7	843	4	US-10-436-715-38	Sequence 38, Appl
30	3231	72.7	843	4	US-10-436-715-70	Sequence 70, Appl
31	3231	72.7	843	4	US-10-725-103-17	Sequence 17, Appl

32	3231	72.7	843	4	US-10-725-489-17	Sequence 17, Appl
33	3231	72.7	843	4	US-10-725-080A-17	Sequence 17, Appl
34	3231	72.7	843	4	US-10-725-472A-17	Sequence 17, Appl
35	3231	72.7	843	5	US-10-725-418-17	Sequence 17, Appl
36	3231	72.7	843	5	US-10-679-102-7	Sequence 7, Appli
37	3231	72.7	843	5	US-10-645-441-7	Sequence 7, Appli
38	3231	72.7	843	5	US-10-725-475-17	Sequence 17, Appl
39	3179	71.6	843	3	US-09-927-315-8	Sequence 8, Appli
40	3179	71.6	843	4	US-10-124-598-2	Sequence 2, Appli
41	3179	71.6	843	4	US-10-096-144-2	Sequence 2, Appli
42	3179	71.6	843	4	US-10-190-417-8	Sequence 8, Appli
43	3179	71.6	843	5	US-10-679-102-8	Sequence 8, Appli
44	3179	71.6	843	5	US-10-645-441-8	Sequence 8, Appli
45	2532.5	57.0	661	4	US-10-246-785-5	Sequence 5, Appli

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OM protein - protein search, using sw model

Run on: June 20, 2006, 18:12:21 ; Search time 22 Seconds  
(without alignments)  
860.228 Million cell updates/sec

Title: US-10-035-045-21  
Perfect score: 4443  
Sequence: 1 MGPRAKTICSLFFLLWVLAE.....ERNTPAYFNSMIQGYTMRRD 839

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 96747 seqs, 22556637 residues

Total number of hits satisfying chosen parameters: 96747

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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8: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US60\_NEW\_PUB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	309.5	7.0	364	7	US-11-293-697-4612 Sequence 4612, Ap
2	239.5	5.4	944	6	US-10-449-902-46707 Sequence 46707, A
3	235.5	5.3	637	6	US-10-449-902-45350 Sequence 45350, A
4	199	4.5	500	6	US-10-449-902-52670 Sequence 52670, A
5	163	3.7	845	6	US-10-449-902-52662 Sequence 52662, A
6	104	2.3	1791	7	US-11-313-450-18 Sequence 18, Appl
7	101.5	2.3	517	6	US-10-449-902-50110 Sequence 50110, A
8	101.5	2.3	595	6	US-10-449-902-42611 Sequence 42611, A
9	97	2.2	416	6	US-10-953-349-5363 Sequence 5363, Ap
10	97	2.2	467	6	US-10-953-349-5362 Sequence 5362, Ap
11	97	2.2	592	6	US-10-953-349-5361 Sequence 5361, Ap
12	95	2.1	764	6	US-10-449-902-42792 Sequence 42792, A
13	94.5	2.1	932	6	US-10-449-902-35289 Sequence 35289, A
14	94.5	2.1	932	6	US-10-449-902-55200 Sequence 55200, A
15	94	2.1	950	6	US-10-449-902-52175 Sequence 52175, A
16	92.5	2.1	500	6	US-10-449-902-28844 Sequence 28844, A
17	92.5	2.1	580	6	US-10-449-902-43846 Sequence 43846, A
18	92	2.1	832	6	US-10-449-902-53946 Sequence 53946, A
19	91	2.0	447	6	US-10-471-571A-5314 Sequence 5314, Ap
20	90	2.0	691	6	US-10-511-937-2995 Sequence 2995, Ap
21	89.5	2.0	382	6	US-10-449-902-50854 Sequence 50854, A
22	89.5	2.0	403	6	US-10-505-928-203 Sequence 203, App
23	89.5	2.0	435	6	US-10-471-571A-2012 Sequence 2012, Ap
24	88.5	2.0	827	6	US-10-449-902-47927 Sequence 47927, A
25	88.5	2.0	858	7	US-11-293-697-2979 Sequence 2979, Ap
26	88.5	2.0	1033	6	US-10-449-902-55424 Sequence 55424, A
27	88	2.0	466	6	US-10-471-571A-5276 Sequence 5276, Ap
28	88	2.0	691	7	US-11-337-061-4 Sequence 4, Appli
29	87.5	2.0	412	6	US-10-449-902-31469 Sequence 31469, A

30	87.5	2.0	565	6	US-10-449-902-44962	Sequence 44962, A
31	87.5	2.0	630	7	US-11-313-450-34	Sequence 34, Appl
32	87	2.0	207	6	US-10-449-902-48804	Sequence 48804, A
33	87	2.0	430	6	US-10-953-349-20015	Sequence 20015, A
34	87	2.0	462	6	US-10-953-349-20014	Sequence 20014, A
35	87	2.0	477	6	US-10-953-349-20013	Sequence 20013, A
36	87	2.0	585	6	US-10-449-902-52644	Sequence 52644, A
37	87	2.0	2937	6	US-10-480-962-18	Sequence 18, Appl
38	87	2.0	2969	6	US-10-480-962-19	Sequence 19, Appl
39	86.5	1.9	369	7	US-11-293-697-3609	Sequence 3609, Ap
40	86.5	1.9	504	6	US-10-505-928-42	Sequence 42, Appl
41	86.5	1.9	788	6	US-10-449-902-48805	Sequence 48805, A
42	86.5	1.9	981	6	US-10-471-571A-666	Sequence 666, App
43	86	1.9	385	6	US-10-449-902-49336	Sequence 49336, A
44	86	1.9	454	6	US-10-449-902-49028	Sequence 49028, A
45	86	1.9	542	7	US-11-261-673-2	Sequence 2, Appli

# SCORE Search Results Details for Application 10035045 and Search Result us-10-035-045-21.rapm.

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[Comments / Suggestions](#)

This page gives you Search Results detail for the Application 10035045 and Search Result us-10-035-045-21.rapm.

[start](#)

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OM protein - protein search, using sw model

Run on: June 20, 2006, 18:00:30 ; Search time 612 Seconds  
(without alignments)  
2093.327 Million cell updates/sec

Title: US-10-035-045-21  
Perfect score: 4443  
Sequence: 1 MGPRAKTICSLFFLLWVLAE.....ERNTPAYFNSMIQGYTMRRD 839

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 8366291 seqs, 1526956180 residues

Total number of hits satisfying chosen parameters: 8366291

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	4443	100.0	839	1	PCT-US04-02987-198	Sequence 198, App
2	4443	100.0	839	1	PCT-US04-25459-6	Sequence 6, Appli
3	4443	100.0	839	1	PCT-US04-32678-29	Sequence 29, Appl
4	4443	100.0	839	30	US-10-035-045-21	Sequence 21, Appl
5	4443	100.0	839	31	US-10-179-373-6	Sequence 6, Appli
6	4443	100.0	839	36	US-10-679-102-29	Sequence 29, Appl
7	4443	100.0	839	37	US-10-725-037-6	Sequence 6, Appli
8	4443	100.0	839	37	US-10-725-080A-6	Sequence 6, Appli
9	4443	100.0	839	37	US-10-725-103-6	Sequence 6, Appli
10	4443	100.0	839	37	US-10-725-276-21	Sequence 21, Appl
11	4443	100.0	839	37	US-10-725-284-21	Sequence 21, Appl
12	4443	100.0	839	37	US-10-725-418-6	Sequence 6, Appli
13	4443	100.0	839	37	US-10-725-472A-6	Sequence 6, Appli
14	4443	100.0	839	37	US-10-725-475-6	Sequence 6, Appli
15	4443	100.0	839	37	US-10-725-488-6	Sequence 6, Appli
16	4443	100.0	839	37	US-10-725-489-6	Sequence 6, Appli
17	4443	100.0	839	40	US-11-050-804-4	Sequence 4, Appli
18	4443	100.0	839	49	US-60-482-992-20	Sequence 20, Appl
19	4443	100.0	839	50	US-60-554-751-20	Sequence 20, Appl
20	4443	100.0	839	52	US-60-710-726-2	Sequence 2, Appli
21	4443	100.0	839	52	US-60-751-420-42	Sequence 42, Appl
22	4423	99.5	839	52	US-60-793-521-10	Sequence 10, Appl
23	4423	99.5	839	52	US-60-793-686-2	Sequence 2, Appli
24	4422	99.5	839	32	US-10-246-785-4	Sequence 4, Appli
25	4392.5	98.9	838	1	PCT-US02-21269-9	Sequence 9, Appli
26	4392.5	98.9	838	1	PCT-US04-32678-9	Sequence 9, Appli
27	4392.5	98.9	838	29	US-09-927-315-9	Sequence 9, Appli
28	4392.5	98.9	838	31	US-10-190-417-9	Sequence 9, Appli
29	4392.5	98.9	838	36	US-10-645-441-9	Sequence 9, Appli
30	4392.5	98.9	838	36	US-10-679-102-9	Sequence 9, Appli
31	4146.5	93.3	838	1	PCT-US04-25459-16	Sequence 16, Appl
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33	3597	81.0	678	31	US-10-170-205E-26489	Sequence 26489, A
34	3597	81.0	678	47	US-60-245-225-365	Sequence 365, App
35	3597	81.0	678	49	US-60-452-680-21000	Sequence 21000, A
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37	3597	81.0	678	49	US-60-453-135-12736	Sequence 12736, A
38	3597	81.0	678	49	US-60-466-412-12736	Sequence 12736, A
39	3564	80.2	682	47	US-60-248-505-716	Sequence 716, App
40	3506	78.9	843	1	PCT-US04-25459-23	Sequence 23, Appl
41	3495.5	78.7	844	1	PCT-US04-25459-17	Sequence 17, Appl



42	3463.5	78.0	669	30	US-10-096-144-7	Sequence 7, Appli
43	3463.5	78.0	669	31	US-10-124-598-7	Sequence 7, Appli
44	3463.5	78.0	669	32	US-10-225-567A-683	Sequence 683, App
45	3398.5	76.5	840	1	PCT-US04-25459-26	Sequence 26, Appl

## ALIGNMENTS

## RESULT 1

PCT-US04-02987-198

; Sequence 198, Application PC/TUS0402987

; GENERAL INFORMATION:

; APPLICANT: SENOMYX, INC.

; TITLE OF INVENTION: FUNCTIONAL COUPLING OF T1RS AND T2RS BY GI PROTEINS

; TITLE OF INVENTION: AND CELL-BASED ASSAYS FOR THE IDENTIFICATION OF T1R

; TITLE OF INVENTION: AND T2R MODULATORS

; FILE REFERENCE: 100337.54281WO

; CURRENT APPLICATION NUMBER: PCT/US04/02987

; CURRENT FILING DATE: 2004-02-03

; PRIOR APPLICATION NUMBER: 60/444,172

; PRIOR FILING DATE: 2003-02-03

; PRIOR APPLICATION NUMBER: 60/457,318

; PRIOR FILING DATE: 2003-03-26

; NUMBER OF SEQ ID NOS: 210

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 198

; LENGTH: 839

; TYPE: PRT

; ORGANISM: Homo sapiens

PCT-US04-02987-198

Query Match 100.0%; Score 4443; DB 1; Length 839;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 839; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MGPRAKTICSLFFLLWVLAEPANSDFYLP GDYLLGGLFSLHANMKGIVHLNFLQVPMCK	60
Db	1	MGPRAKTICSLFFLLWVLAEPANSDFYLP GDYLLGGLFSLHANMKGIVHLNFLQVPMCK	60
Qy	61	EYEVKVI GYNLMQAMRFAVEEINNDSSLLPGVLLGYEIVDVCYISNNVQPVLYFLAHEDN	120
Db	61	EYEVKVI GYNLMQAMRFAVEEINNDSSLLPGVLLGYEIVDVCYISNNVQPVLYFLAHEDN	120
Qy	121	LLPIQEDYSNYISR VVAVIGPDNSESVM TVANFLSLFLLPQITYSAISDEL RDKVRFPAL	180
Db	121	LLPIQEDYSNYISR VVAVIGPDNSESVM TVANFLSLFLLPQITYSAISDEL RDKVRFPAL	180
Qy	181	LRTTPSADHHVEAMVQLMLHFRWNWIIIVLVSSDTYGRDNGQLLGERVARRD ICIAFQETL	240
Db	181	LRTTPSADHHVEAMVQLMLHFRWNWIIIVLVSSDTYGRDNGQLLGERVARRD ICIAFQETL	240
Qy	241	PTLQPNQNM TSEERQRLVTIVDKLQQSTARVV VVFPDLTLYHFFNEVLRQNFTGAVWIA	300
Db	241	PTLQPNQNM TSEERQRLVTIVDKLQQSTARVV VVFPDLTLYHFFNEVLRQNFTGAVWIA	300
Qy	301	SESWAIDPVLHNLTELGH LGTFLGITI QSVPIPGFSEFREWGPQAGPPPLSRTS QS SYTCN	360
Db	301	SESWAIDPVLHNLTELGH LGTFLGITI QSVPIPGFSEFREWGPQAGPPPLSRTS QS SYTCN	360
Qy	361	QEC DNCLNATLSFN TILRLSGERVVYSVYSAVYAVAHALHSL LGCDKSTCTKR VVYPWQL	420
Db	361	QEC DNCLNATLSFN TILRLSGERVVYSVYSAVYAVAHALHSL LGCDKSTCTKR VVYPWQL	420
Qy	421	LEEIWKNFTLLDHQIFFDPQGDVALHLEIVQWQWDRSQNPFSVASYYPLQRQLKNIQD	480
Db	421	LEEIWKNFTLLDHQIFFDPQGDVALHLEIVQWQWDRSQNPFSVASYYPLQRQLKNIQD	480
Qy	481	ISWHTVNNTIPMSMCSKRCQSGQKKKPVGIHVCCFECIDCLPGTFLNHTEDEYECQACPN	540
Db	481	ISWHTVNNTIPMSMCSKRCQSGQKKKPVGIHVCCFECIDCLPGTFLNHTEDEYECQACPN	540
Qy	541	NEWSYQSETSCFKRQLVFLEWHEAPTIAVALLAALGFLSTLAILVIFWRHFQTPIVRSAG	600
Db	541	NEWSYQSETSCFKRQLVFLEWHEAPTIAVALLAALGFLSTLAILVIFWRHFQTPIVRSAG	600



[illegible]

## RESULT 2

PCT-US04-25459-6

; Sequence 6, Application PC/TUS0425459

; GENERAL INFORMATION:

; APPLICANT: Senomyx, Inc.

; TITLE OF INVENTION: T1R HETERO-OLIGOMERIC TASTE RECEPTORS,

; TITLE OF INVENTION: CELL LINES THAT EXPRESS SAID RECEPTORS, AND TASTE COMPOUNDS

```

; FILE REFERENCE: 19328.0001P1

```

: CURRENT APPLICATION NUMBER: PCT/US04/25459

CURRENT FILING DATE: 2004-08-06

: PRIOR APPLICATION NUMBER: 60/494,071

; PRIOR FILING DATE: 2003-08-06

: PRIOR APPLICATION NUMBER: 60/552,064

: PRIOR FILING DATE: 2004-03-09

: NUMBER OF SEO ID NOS: 33

```

; SOFTWARE: FastSEO for Windows Version 4.0

```

; SEQ ID NO 6

```

; SEQ ID NO 8
;   LENGTH: 839

```

; TYPE: PRT

```
; TYPE: PRI
; ORGANISM: Artificial Sequence
```

: FEATURE:

```

; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence; note =

```

: OTHER INFORMATION: synthetic construct

PCT-US04-25459-6

Query Match 100.0%; Score 4443; DB 1; Length 839;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 839; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MGPRAKTICSLFFLLWVLAEPAENSDFYLPGDYLLGGFLSLHANMKGIVHLNFLQVPMCK	60
Db	1	MGPRAKTICSLFFLLWVLAEPAENSDFYLPGDYLLGGFLSLHANMKGIVHLNFLQVPMCK	60
Qy	61	EYEVKVGIGYNLMQAMRFAVEEINNDSSLLPGVLLGYEIVDVCYISNNVQPVLYFLAHEDN	120
Db	61	EYEVKVGIGYNLMQAMRFAVEEINNDSSLLPGVLLGYEIVDVCYISNNVQPVLYFLAHEDN	120
Qy	121	LLPIQEDYSNYISRVAVIGPDNSESVMTVANFLSLFLLPQITYSAISDELDRDKVRFPAL	180
Db	121	LLPIQEDYSNYISRVAVIGPDNSESVMTVANFLSLFLLPQITYSAISDELDRDKVRFPAL	180
Qy	181	LRTTPSADHHVEAMVQLMLHFRWNWIIIVLVSSDITYGRDNGQLLGERVARRDICIAFQETL	240
Db	181	LRTTPSADHHVEAMVQLMLHFRWNWIIIVLVSSDITYGRDNGQLLGERVARRDICIAFQETL	240
Qy	241	PTLQPNQNMNTSEERQRLVTIVDKLQQSTARVVVFSPDLTLYHFFNEVLRQNFTGAVWIA	300
Db	241	PTLQPNQNMNTSEERQRLVTIVDKLQQSTARVVVFSPDLTLYHFFNEVLRQNFTGAVWIA	300
Qy	301	SESWAIDPVLHNLTELGHGLGTFLGITIQSVPIPGFSEFREWGPQAGPPPLSRTSQQSYTCN	360
Db	301	SESWAIDPVLHNLTELGHGLGTFLGITIQSVPIPGFSEFREWGPQAGPPPLSRTSQQSYTCN	360
Qy	361	QECNCLNATLSFNITILRLSGERVVYSVYSAVYAVAHALHSLGCDKSTCTKRVVYPWQL	420
Db	361	QECNCLNATLSFNITILRLSGERVVYSVYSAVYAVAHALHSLGCDKSTCTKRVVYPWQL	420
Qy	421	LEEIWKNVFTLLDHQIFFDPQGDVALHLEIVQWQWDRSQNPFSVASYYPLQRQLKNIQD	480
Db	421	LEEIWKNVFTLLDHQIFFDPQGDVALHLEIVQWQWDRSQNPFSVASYYPLQRQLKNIQD	480

OM protein - protein search, using sw model

Run on: June 20, 2006, 18:01:30 ; Search time 26 Seconds  
(without alignments)  
1101.734 Million cell updates/sec

Title: US-10-035-045-21  
Perfect score: 4443  
Sequence: 1 MGPRAKTICSLFLLWVLAE.....ERNTPAYFNSMIQGYTMRRD 839

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 142608 seqs, 34141942 residues

Total number of hits satisfying chosen parameters: 142608

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Pending\_Patents\_AA\_New:\*  
1: /EMC\_Celerra\_SIDS3/ptodata/2/paa/PCT\_NEW\_COMB.pep:\*  
2: /EMC\_Celerra\_SIDS3/ptodata/2/paa/US06\_NEW\_COMB.pep:\*  
3: /EMC\_Celerra\_SIDS3/ptodata/2/paa/US07\_NEW\_COMB.pep:\*  
4: /EMC\_Celerra\_SIDS3/ptodata/2/paa/US08\_NEW\_COMB.pep:\*  
5: /EMC\_Celerra\_SIDS3/ptodata/2/paa/US09\_NEW\_COMB.pep:\*  
6: /EMC\_Celerra\_SIDS3/ptodata/2/paa/US10\_NEW\_COMB.pep:\*  
7: /EMC\_Celerra\_SIDS3/ptodata/2/paa/US11\_NEW\_COMB.pep:\*  
8: /EMC\_Celerra\_SIDS3/ptodata/2/paa/US60\_NEW\_COMB.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

		%						
Result		Query						Description
No.	Score	Match	Length	DB	ID			
1	1089	24.5	1027	7	US-11-446-813-2	Sequence 2, Appli		
2	1079.5	24.3	1078	7	US-11-242-079-7	Sequence 7, Appli		
3	1075	24.2	1079	7	US-11-242-079-8	Sequence 8, Appli		
4	1075	24.2	1085	7	US-11-242-079-5	Sequence 5, Appli		
5	1065.5	24.0	1078	7	US-11-446-813-30	Sequence 30, Appl		
6	1064.5	24.0	1088	7	US-11-242-079-6	Sequence 6, Appli		
7	1051	23.7	941	7	US-11-446-813-8	Sequence 8, Appli		
8	1051	23.7	941	7	US-11-446-813-14	Sequence 14, Appl		
9	1044	23.5	941	7	US-11-446-813-10	Sequence 10, Appl		
10	1020	23.0	850	7	US-11-446-813-12	Sequence 12, Appl		
11	404.5	9.1	388	7	US-11-446-813-6	Sequence 6, Appli		
12	248.5	5.6	197	7	US-11-446-813-4	Sequence 4, Appli		
13	180	4.1	960	7	US-11-317-847A-108	Sequence 108, App		
14	180	4.1	979	7	US-11-317-847A-172	Sequence 172, App		
15	180	4.1	1033	7	US-11-317-847A-174	Sequence 174, App		
16	130.5	2.9	885	1	PCT-US06-16533-7	Sequence 7, Appli		
17	129.5	2.9	938	6	US-10-222-772A-14	Sequence 14, Appl		
18	126	2.8	1007	6	US-10-578-392-13	Sequence 13, Appl		
19	119.5	2.7	1002	7	US-11-431-708-355	Sequence 355, App		
20	119.5	2.7	1004	7	US-11-431-708-358	Sequence 358, App		
21	119.5	2.7	1013	7	US-11-431-708-359	Sequence 359, App		
22	119.5	2.7	1013	7	US-11-431-708-360	Sequence 360, App		
23	113	2.5	471	7	US-11-431-855-11909	Sequence 11909, A		
24	113	2.5	471	7	US-11-431-855-20499	Sequence 20499, A		
25	104.5	2.4	2478	7	US-11-431-855-17636	Sequence 17636, A		
26	103	2.3	1970	6	US-10-418-772-1	Sequence 1, Appli		
27	102.5	2.3	488	7	US-11-431-855-28773	Sequence 28773, A		
28	100.5	2.3	441	7	US-11-429-594-86	Sequence 86, Appl		
29	100.5	2.3	488	7	US-11-431-855-23001	Sequence 23001, A		
30	100	2.3	1115	6	US-10-222-772A-16	Sequence 16, Appl		
31	99.5	2.2	376	7	US-11-431-855-4192	Sequence 4192, Ap		
32	99.5	2.2	1390	7	US-11-431-708-861	Sequence 861, App		

33	99.5	2.2	1390	7	US-11-437-729-1183	Sequence 1183, Ap
34	97	2.2	475	6	US-10-392-219A-5	Sequence 5, Appli
35	97	2.2	507	1	PCT-US06-17162-90	Sequence 90, Appl
36	97	2.2	507	7	US-11-417-264-90	Sequence 90, Appl
37	96	2.2	1499	7	US-11-431-855-23601	Sequence 23601, A
38	96	2.2	1515	7	US-11-431-855-11298	Sequence 11298, A
39	95.5	2.1	319	7	US-11-434-137-2602	Sequence 2602, Ap
40	95.5	2.1	319	7	US-11-434-184-2602	Sequence 2602, Ap
41	95.5	2.1	319	7	US-11-434-203-2602	Sequence 2602, Ap
42	95.5	2.1	319	7	US-11-434-127-2602	Sequence 2602, Ap
43	95.5	2.1	319	7	US-11-434-199-2602	Sequence 2602, Ap
44	95.5	2.1	487	7	US-11-431-855-20992	Sequence 20992, A
45	95.5	2.1	1762	7	US-11-431-855-25593	Sequence 25593, A